

Replace the paragraph beginning at page 47, line 19, with the following rewritten paragraph:

D 3 - Fig. 2 is a diagram depicting homology at the amino acid level between the mouse (amino acid residues 275 to 507 of SEQ ID NO:2) and chicken (SEQ ID NO:30) Aiolos sequence and the mouse (amino acid residues 283 to 518 of SEQ ID NO:27) and chicken Ikaros exon 7 (SEQ ID NO:31) sequence.

Replace the paragraph beginning at page 47, line 22, with the following rewritten paragraph:

D 4 - Fig. 3 is a diagram depicting the homology between mouse Aiolos amino acid sequence (amino acid residues 109 to 305 of SEQ ID NO:2) and mouse Ikaros amino acid sequence (amino acid residues 1 to 310 of SEQ ID NO:27).

Replace the paragraph beginning at page 47, line 25, with the following rewritten paragraph:

D 5 - Fig. 4 is a diagram depicting Aiolos exons (exon 3: SEQ ID NO:32; exon 4: SEQ ID NO:33; exon 5: SEQ ID NO:34; exon 6: SEQ ID NO:35; exon 7: SEQ ID NO:36). Based on homology to Ikaros, the exons encoding different segments of the Aiolos gene are deduced. The exon boundaries of exons 5/6 and 6/7 have been confirmed from genomic sequence (6/7) or from differential splice products (5/6). Three classes of cDNA were recovered. The first contains exons 3 through 7. A second class splices exon 5 directly to exon 7, skipping exon 6. The third contains exon 7 and contiguous genomic sequence extending upstream of this exon.

Replace the paragraph beginning at page 47, line 32, with the following rewritten paragraph:

D 6 - Fig. 5A: is a human Aiolos cDNA nucleotide sequence. Consensus sequence of human Aiolos cDNA from RTPCR using mouse AioF primer (ex3) in forward direction and human hAio2 primer (ex6) in reverse direction. This sequence does not include the AioF primer sequence but does include the hAio2 sequence. AioF = atg aaa gtg aaa gat gaa tac agc (SEQ ID NO:38) only human sequence is shown here. EcoRI sites flank directly 5' and 3'. The cDNA sequence in figure 5A is SEQ ID NO: 7. 5B: shows a corresponding human amino acid

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sequence 209 amino acids in length (SEQ ID NO:8). 5B also shows the corresponding mouse sequence and shows regions of shared sequence (amino acid residues 66 to 273 of SEQ ID NO:2). The consensus sequence in 5B is SEQ ID NO:37.

Replace the paragraph beginning at page 48, line 4, with the following rewritten paragraph:

D 7
-Fig. 6 is a diagram depicting comparison of the amino acid sequence of Aiolos (top sequence; SEQ ID NO:2) and Ikaros (bottom sequence; SEQ ID NO:27) proteins. The boxed methionines represent the three translation initiation codons. The boxed cysteines and histidines represent the paired cysteines and histidines of the zinc finger motifs. The conserved activation domain (amino acids 290-344 of Aiolos protein) is shaded. Identical residues are indicated by bars and conservative residues are indicated by dots.